



#2 OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/092,404

DATE: 04/09/2002

TIME: 10:51:10

Input Set : N:\Crf3\RULE60\10092404.raw

Output Set: N:\CRF3\04092002\J092404.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Feder, John N.

6 Bjorkman, Pamela J.

7 Schatzman, Randall C.

9 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
10 DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
11 AND IRON DEFICIENCY DISEASES

13 (iii) NUMBER OF SEQUENCES: 5

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Pennie & Edmonds, LLP

17 (B) STREET: 1155 Avenue of the Americas

18 (C) CITY: New York

19 (D) STATE: NY

20 (E) COUNTRY: USA

21 (F) ZIP: 10036-2811

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette

25 (B) COMPUTER: IBM Compatible

26 (C) OPERATING SYSTEM: Windows

27 (D) SOFTWARE: FastSEQ for Windows Version 2.0b

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/10/092,404

C--> 31 (B) FILING DATE: 04-Mar-2002

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/09/094,964

36 (B) FILING DATE: June 12, 1998

38 (A) APPLICATION NUMBER: 08/876,010

39 (B) FILING DATE: June 13, 1997

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Poissant, Brian M

45 (B) REGISTRATION NUMBER: 28,462

46 (C) REFERENCE/DOCKET NUMBER: 8907-0074-999

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 650-493-4935

50 (B) TELEFAX: 650-493-5556

51 (C) TELEX: 66141 PENNIE

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 276 amino acids

58 (B) TYPE: amino acid

59 (C) STRANDEDNESS: single

ENTERED

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60      (D) TOPOLOGY: linear
62      (ii) MOLECULE TYPE: peptide
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66  Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser
67   1          5          10          15
68  Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
69   20          25          30
70  Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro
71   35          40          45
72  Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln
73   50          55          60
74  Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
75   65          70          75          80
76  Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu
77   85          90          95
78  Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
79   100         105         110
80  Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro
81   115         120         125
82  Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
83   130         135         140
84  Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
85   145         150         155         160
86  Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Leu Leu Glu Leu Gly
87   165         170         175
88  Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His
89   180         185         190
90  His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr
91   195         200         205
92  Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met
93   210         215         220
94  Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly
95   225         230         235         240
96  Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln
97   245         250         255
98  Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile
99   260         265         270
100 Val Ile Trp Glu
101   275
103 (2) INFORMATION FOR SEQ ID NO: 2:
105      (i) SEQUENCE CHARACTERISTICS:
106          (A) LENGTH: 276 amino acids
107          (B) TYPE: amino acid
108          (C) STRANDEDNESS: single
109          (D) TOPOLOGY: linear
111      (ii) MOLECULE TYPE: peptide
113      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
115  Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser
116   1          5          10          15

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```

117 Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
118           20           25           30
119 Asp Gln Leu Phe Val Phe Tyr Asp Asp Glu Ser Arg Arg Val Glu Pro
120           35           40           45
121 Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln
122           50           55           60
123 Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
124           65           70           75           80
125 Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu
126           85           90           95
127 Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
128           100          105          110
129 Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro
130           115          120          125
131 Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
132           130          135          140
133 Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
134           145          150          155          160
135 Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly
136           165          170          175
137 Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His
138           180          185          190
139 His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr
140           195          200          205
141 Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met
142           210          215          220
143 Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly
144           225          230          235          240
145 Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln
146           245          250          255
147 Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile
148           260          265          270
149 Val Ile Trp Glu
150           275

```

152 (2) INFORMATION FOR SEQ ID NO: 3:

154 (i) SEQUENCE CHARACTERISTICS:

155 (A) LENGTH: 276 amino acids

156 (B) TYPE: amino acid

157 (C) STRANDEDNESS: single

158 (D) TOPOLOGY: linear

160 (ii) MOLECULE TYPE: peptide

162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

164 Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser
165   1       5       10       15
166 Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
167           20           25           30
168 Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro
169           35           40           45
170 Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln

```

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Output Set: N:\CRF3\04092002\J092404.raw

```

171      50      55      60
172 Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
173 65      70      75      80
174 Trp Thr Ile Met Glu Asn His Asn Ala Ser Lys Glu Ser His Thr Leu
175      85      90      95
176 Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
177      100      105      110
178 Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp Ala Leu Glu Phe Cys Pro
179      115      120      125
180 Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
181      130      135      140
182 Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
183 145      150      155      160
184 Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly
185      165      170      175
186 Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His
187      180      185      190
188 His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr
189      195      200      205
190 Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met
191      210      215      220
192 Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly
193 225      230      235      240
194 Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln
195      245      250      255
196 Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile
197      260      265      270
198 Val Ile Trp Glu
199      275

```

201 (2) INFORMATION FOR SEQ ID NO: 4:

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 12 amino acids

205 (B) TYPE: amino acid

206 (C) STRANDEDNESS: single

207 (D) TOPOLOGY: linear

W--> 209 (ii) MOLECULE TYPE: None

211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

213 Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe

214 1 5 10

216 (2) INFORMATION FOR SEQ ID NO: 5:

218 (i) SEQUENCE CHARACTERISTICS:

219 (A) LENGTH: 12 amino acids

220 (B) TYPE: amino acid

221 (C) STRANDEDNESS: single

222 (D) TOPOLOGY: linear

W--> 224 (ii) MOLECULE TYPE: None

226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

228 Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg

229 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/092,404

DATE: 04/09/2002

TIME: 10:51:11

Input Set : N:\Crf3\RULE60\10092404.raw

Output Set: N:\CRF3\04092002\J092404.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:209 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4

L:224 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5